In the Specification:

Please replace the paragraph beginning at page 4, line 2, with the following:

B1

--Figure 1 shows the nucleic acid sequence of a vector encoding TbF14 (SEQ ID NO:91). Nucleotides 5096 to 8594 encode TbF14 (SEQ ID NO:51). Nucleotides 5072 to 5095 encode the eight amino acid His tag (SEQ ID NO:92); nucleotides 5096 to 7315 encode the MTb81 antigen (SEQ ID NO:1); and nucleotides 7316 to 8594 encode the Mo2 antigen (SEQ ID NO:3).--

Please replace the paragraph beginning at page 4, line 10, with the following:

B2

--Figure 2 shows the nucleic acid sequence of a vector encoding TbF15 (SEQ ID NO:92). Nucleotides 5096 to 8023 encode the TbF15 fusion protein (SEQ ID NO:53). Nucleotides 5072 to 5095 encode the eight amino acid His tag region; nucleotides 5096 to 5293 encode the Ra3 antigen (SEQ ID NO:5); nucleotides 5294 to 6346 encode the 38 kD antigen (SEQ ID NO:7); nucleotides 6347 to 6643 encode the 38-1 antigen (SEQ ID NO:9); and nucleotides 6644 to 8023 encode the FL TbH4 antigen (SEQ ID NO:11).--

Please replace the paragraph beginning at page 4, line 21, with the following:

B3

--Figure 7 shows the nucleic acid and predicted amino acid sequences of three fragments of HTCC#1. (a) and (b) show the sequences of two overlapping fragments: an amino terminal half fragment (SEQ ID NOS:15 and 16) (residues 1 to 232 223), comprising the first trans-membrane domain (a) and a carboxy terminal half fragment (SEQ ID NOS:17 and 18) (residues 184 to 392), comprising the last two trans-membrane domains (b); (c) shows a truncated amino-terminal half fragment (SEQ ID NOS:19 and 20) (residues 1 to 129 128) devoid of the trans-membrane domain.--

Please replace the paragraph beginning at page 4, line 29, with the following:

B4

--Figure 9a shows the nucleic acid and predicted amino acid sequences of a recombinant HTCC#1 lacking the first trans-membrane domain (SEQ ID NOS:21 and 22) (deleted of the amino acid residues 150 to 160). Figure 9b (SEQ ID NOS:201 and 202) shows the nucleic acid and predicted amino acid sequences of 30 overlapping peptides (SEQ ID NOS:94-123 and 124-153, respectively) of HTCC#1 used for the T-cell epitope mapping. Figure 9c illustrates the results of the T-cell epitope mapping of HTCC#1. Figure 9d shows the nucleic acid and predicted amino acid sequences of a deletion construct of HTCC#1 lacking all the trans-membrane domains (SEQ ID NOS:23 and 24) (deletion of amino acid residues 101 to 203).--

Please replace the paragraph beginning at page 5, line 20, with the following:

B5

--Figure 17 shows the amino acid sequence of *Mycobacterium tuberculosis* the secreted form of antigen DPPD (SEQ ID NO:154).--

Please replace the paragraph beginning at page 6, line 7, with the following:

B6

--SEQ ID NO:15 is the nucleic acid sequence of an amino terminal half fragment (residues 1 to 232) of HTCC#1, comprising the first trans-membrane domain.--

Please replace the paragraph beginning at page 6, line 9, with the following:

B7

--SEQ ID NO:16 is the predicted amino acid sequence of an amino terminal half fragment (residues 1 to 232) of HTCC#1.--

Please replace the paragraph beginning at page 6, line 16, with the following:

B8 --SEQ ID NO:19 is the nucleic acid sequence of a truncated amino-terminal half fragment (residues 1 to 129) of HTCC#1 devoid of the trans-membrane domain.--

Please replace the paragraph beginning at page 6, line 18, with the following:

B9 --SEQ ID NO:20 is the predicted amino acid sequence of a truncated amino-terminal half fragment (residues 1 to 129) of HTCC#1.--

Please replace the paragraph beginning at page 7, line 8, with the following:

B10 --SEQ ID NO:33 is the nucleic acid sequence encoding the MTI (Mtb9.9A) antigen. SEQ ID NO:155 is a second nucleic acid sequence encoding the MTI (Mtb9.9A) antigen.--

Please replace the paragraph beginning at page 7, line 10, with the following:

B11 --SEQ ID NO:34 is the amino acid sequence of the MTI antigen. Mtb9.9A (MTI-A) ORF peptides are given in SEQ ID NOS:156-171.--

Please replace the paragraph beginning at page 7, line 13, with the following:

B12 --SEQ ID NO:36 is the amino acid sequence of the MSL antigen. Mtb9.8 (MSL) ORF peptides are given in SEQ ID NOS:172-186.--

Please replace the paragraph beginning at page 72, line 17, with the following:

B 13

--TbF14 is a fusion protein of the amino acid sequence encoding the MTb81 antigen fused to the amino acid sequence encoding the Mo2 antigen. A sequence encoding Mo2 was PCR amplified with the following primers: PDM-294 (T_m 64°C) CGTAATCACGTGCAGAAGTACGGCGGATC (SEQ ID NO:187) and PDM-295 (T_m 63°C) CCGACTAGAATTCACTATTGACAGGCCCATC (SEQ ID NO:188).--

Please replace the paragraph beginning at page 72, line 27, with the following:

B 14

--A sequence encoding MTb81 was PCR amplified with the following primers: PDM-268 (T_m 66°C) CTAAGTAGTACTGATCGCGTGTCGGTGGGC (SEQ ID NO:189) and PDM-296 (T_m 64°C) CATCGATAGGCCTGGCCGCATCGTCACC (SEQ ID NO:190). The amplification reaction was performed using the same mix as above, as follows: denaturation at 96°C for 2 min; followed by 40 cycles of 96°C for 20 sec, 65°C for 15 sec, 72°C for 5 min; and finally by 72°C for 5 min.--

Please replace the paragraph beginning at page 73, line 12, with the following:

B 15

--TbF6 was made as follows (see PCT/US99/03268 and PCT/US99/03265). First, the FL (full-length) TbH4 coding region was PCR amplified with the following primers:PDM-157 CTAGTTAGTACTCAGTCGCAGACCGTG (SEQ ID NO:191) (T_m 61°C) and PDM-160 GCAGTGACGAATTCACTTCGACTCC (SEQ ID NO:192) (T_m 59°C), using the following conditions: 10 µl 10X Pfu buffer, 1µl 10 mM dNTPs, 2 µl 10 µM each oligo, 82 µl sterile water, 1.5 µl Accuzyme (ISC, Kaysville, UT), 200 ng *Mycobacterium tuberculosis* genomic DNA. Denaturation at 96°C was performed for 2 minutes; followed by 40 cycles of 96°C for 20 seconds, 61°C 15 seconds, and 72°C 5 minutes; and finally by 72°C 10 minutes.--

Please replace the paragraph beginning at page 73, line 23, with the following:

--pET28Ra3/38kD/38-1A was made by inserting a DraI site at the end of 38-1 before the stop codon using the following conditions. The 38-1 coding region was PCR amplified with the following primers: PDM-69 GGATCCAGCGCTGAGATGAAGACCGATGCCGCT (SEQ ID NO:193) (T_m 68°C) and PDM-83 GGATATCTGCAGAATTCAGGTTTAAAGCCCATTTGCGA (SEQ ID NO:194) (T_m 64°C), using the following conditions: 10 µl 10X Pfu buffer, 1 µl 10 mM dNTPs, 2 µl 10 µM each oligo, 82 µl sterile water, 1.5 µl Accuzyme (ISC, Kaysville, UT), 50 ng plasmid DNA. Denaturation at 96°C was performed for 2 minutes; followed by forty cycles of 96°C for 20 seconds, 66°C for 15 seconds and 72°C for 1 minute 10 seconds; and finally 72°C 4 minutes.--

B16

Please replace the paragraph beginning at page 74, line 7, with the following:

--Fusion construct TbF10, which replaces the N-terminal cysteine of 38 kD, was made as follows. To replace the cysteine residue at the N-terminus, the 38kD-38-1 coding region from the TbF fusion (described in WO/9816646 and WO/9816645) was amplified using the following primers: PDM-192 TGTGGCTCGAAACCACCGAGCGGTTC (SEQ ID NO:195) (T_m 64°C) and PDM-60 GAGAGAATTCTCAGAAGCCCATTTGCGAGGACA (SEQ ID NO:196) (T_m 64°C), using the following conditions: 10 µl 10X Pfu buffer, 1 µl 10 mM dNTPs, 2 µl 10 µM each oligo, 83 µl sterile water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA), and 50 ng plasmid TbF DNA. The amplification reaction was performed as follows: 96°C for 2 minutes; followed by 40 cycles of 96°C for 20 seconds, 64°C 15 seconds, and 72°C 4 minutes; and finally 72°C 4 minutes. Digest the PCR product with Eco RI and clone into pT7ΔL2Ra3 which has been digested with Stu I and Eco RI. Digest the resulting construct with Nde I and EcoRI and clone into pET28 at those sites. The

B17

resulting clone (called TbF10) will be TBF + a cysteine at the 5' end of the 38kD coding region. Transform into BL21 and HMS 174 with pLys S--

Please replace the paragraph beginning at page 77, line 14, with the following:

--One of the identified positive wells was further broken down until a single reactive clone (HTCC#l) was identified. Sequencing of the DNA insert followed by search of the Genebank database revealed a 100% identity to sequences within the *M. tuberculosis* locus MTCY7H7B (gene identification MTCY07H7B.06) located on region B of the cosmid clone SCY07H7. The entire open reading frame is ~1,200 bp long and codes for a 40 kDa (392 amino acids) protein (Fig. 1; HTCC#1 FL). Oligonucleotide PCR primers [5'(5'-CAA TTA CAT ATG CAT CAC CAT CAC CAT CAC *ATG AGC AGA GCG TTC ATC ATC*-3'; SEQ ID NO:197) and 3' (5'-CAT GGA ATT CGC CGT TAG ACG ACG TTT CGT A-3'; SEQ ID NO:198)] were designed to amplify the full-length sequence of HTCC#1 from genomic DNA of the virulent Erdman strain.--

B 18

Please replace the paragraph beginning at page 78, line 27, with the following:

--Specifically, the C-terminal fragment of antigen MTB32A was amplified by standard PCR methods using the oligonucleotide primers 5'(CAA TTA CAT ATG CAT CAC CAT CAC CAT CAC *ACG GCC GCG TCC GAT AAC TTC*; SEQ ID NO:199) and 3' (5'-CTA ATC GAA TTC *GGC CGG GGG TCC CTC GGC CAA*; SEQ ID NO:200). The 450 bp product was digested with NdeI and EcoRI and cloned into the pET17b expression vector similarly digested with the same enzymes.--

B 19

Please cancel the informal "SEQUENCE LISTING", pages 1-26, and insert therefor the accompanying paper copy of the Substitute Sequence Listing, page numbers 1 to 119, at the end of the application.